FIG. 1A

```
caggatcag ggttccagga actcaggatc tgcagtgagg accagacacc actgattgca  60

gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat gca   108
    Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
     1               5                  10                  15

gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat   156
Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
                 20                  25                  30

cct gtt gca gac aac tgc tgt gca gag aag atc tgc aca ctt cct aac   204
Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn
             35                  40                  45

aga ggc ttg gac cgc acc aag gtc ccc att ttc ctg ggg atc cag gga   252
Arg Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
         50                  55                  60

ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta   300
Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
     65                  70                  75

cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag   348
Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
 80                  85                  90                  95

gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg   396
Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
                100                 105                 110

ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag   444
Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
            115                 120                 125

ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt   492
Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
        130                 135                 140

acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt   542
Thr Lys Phe Tyr Phe Glu Gln Ser Trp
    145                 150

tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg  602

tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac catacatgtc  662

caaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg  722

ttatccttgt gggctcagtt taatcacaag aaggaggcag gaagggagag tcagagagag  782

aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacaaat  842

gcaggtgttt ttagaaggtg gaaaagccaa gggaacggat tctcctctag agtctccgga  902
```

FIG. 1B

```
aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962

ctccacaact ataaaataat aaacttgtgt tattgtaaac ctctaaaaaa aaaaaaaa   1020
```

FIG. 2A

```
cagggatcag ggttccagga actcaggatc tgcagtgagg accagacacc actgattgca 60

gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa tat gca      108
    Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Tyr Ala
      1               5                  10                  15

gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat      156
Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp
                  20                  25                  30

cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt cct aac      204
Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu Pro Asn
              35                  40                  45

aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc cag gga      252
Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly
          50                  55                  60

ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct tcc cta      300
Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu
      65                  70                  75

cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag      348
Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
 80                  85                  90                  95

gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc ttc agg      396
Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg
                 100                 105                 110

ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg gca gag      444
Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
             115                 120                 125

ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt      492
Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
             130                 135                 140

acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt        542
Thr Lys Phe Tyr Phe Glu Gln Ser Trp
         145                 150

tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg 602

tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac catacatgtc 662

caaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 722

ttatccttgt gggctcagtt taatcacaag aaggaggcag gaagggagag tcagagagag 782

aatggaagat accatgcttc taattttgaa gatggagtga ggggccttga gccaacaaat 842

gcaggtgttt ttagaaggtg gaaaagccaa gggaacggat tctcctctag agtctccgga 902
```

FIG. 2B

```
aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962

ctccacaact ataaaataat aaacttgtgt tattgtaaac tctaaaaaa aaaaaaaa   1020
```
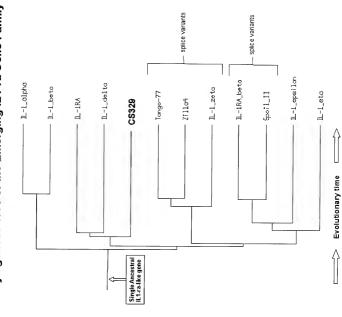
FIG. 3

```
gctcccgcca ggagaaagga acattctgag gggagtctac accctgtgga gctcaag        57

atg gtc ctg agt ggg gcg ctg tgc ttc cgt gag gac cag aca cca ctg      105
Met Val Leu Ser Gly Ala Leu Cys Phe Arg Glu Asp Gln Thr Pro Leu
  1               5                  10                      15

att gca gga atg tgt tcc ctc ccc atg gca aga tac tac ata att aaa      153
Ile Ala Gly Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys
              20                  25                  30

tat gca gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg      201
Tyr Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val
          35                  40                  45

gga gat cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt      249
Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu
      50                  55                  60

cct aac aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc      297
Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile
 65                  70                  75                      80

cag gga ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct      345
Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro
                  85                  90                  95

tcc cta cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt      393
Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly
              100                 105                 110

gaa gag gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc      441
Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala
          115                 120                 125

ttc agg ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc ccg      489
Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro
      130                 135                 140

gca gag ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca      537
Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser
145                 150                 155                 160

gcc cgt acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga          583
Ala Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp
                  165                 170

aactgcgttt tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg   643

cagaataatg tcccccgaaa tatgtccaca tcctaatccc aagatctgtg catatgttac   703

catacatgtc caaagaggtt ttgcaaatgt gattatgtta a                       744
```

FIG. 4A

```
             1                                                    50
  IL-1_alpha  MAEVPKLASE  MMAYYSGNED  DLFFEADGPK  QMKCSFQDLD  LCPLDGGIQL
   IL-1_beta  ----------  ----------  ----------  ----------  ----------
       IL-1RA  ----------  ----------  ----------  ----------  ----------
  IL-1_delta  ----------  ----------  ----------  ----------  ----------
        CS329  ----------  ----------  ----------  ----------  ----------
     Tango-77  ----------  ----------  ----------  ----------  ----------
       Zilla4  ----------  ----------  ----------  ----------  ----------
   IL-1_zeta  ----------  ----------  ----------  ----------  ----------
  IL-1RA_beta  ----------  ----------  ----------  ----------  ----------
     Spoil_II  ----------  ----------  ----------  ----------  ----------
IL-1_epsilon  ----------  ----------  ----------  ----------  ----------
     IL-1_eta  ----------  ----------  ----------  ----------  ----------

             51                                                   100
  IL-1_alpha  RISDHHYSKG  FRQAASVVVA  MDKLRKMLVP  CPQTFQENDL  STFFFPFIFEE
   IL-1_beta  ----------  ----------  ----------  ----------  ----------
       IL-1RA  ----------  ----------  ----------  ------MEIC  RGLRSHLITL
  IL-1_delta  ----------  ----------  ----------  ----------  ----------
        CS329  ----------  ----------  ----------  ----------  ----------
     Tango-77  ----------  --MSFVGENS  GVKMGSEDWE  KDEPQCCLED  PAGSPLEPGP
       Zilla4  ----------  --MSFVGENS  GVKMGSEDWE  KDEPQCCLED  PAGSPLEPGP
   IL-1_zeta  ----------  ----------  ----------  ----------  MSGCDRRETE
  IL-1RA_beta  ----------  MRGTPGDADG  GGRAVYQS..  ..........  ..........
     Spoil_II  ----------  MRGTPGDADG  GGRAVYQSSE  SNAVGMGLWR  LRPSALTLSP
IL-1_epsilon  ----------  ----------  ----------  ----------  ----------
     IL-1_eta  ----------  ----------  ----------  ----------  ----------

             101                                                  150
  IL-1_alpha  EPIFFDTWDN  EAYVHDAPVR  SLNCTLRDSQ  QKSLVMSGPY  ELKALHLQGQ
   IL-1_beta  ----------  ------APVR  SLNCTLRDSQ  QKSLVMSGPY  ELKALHLQGQ
       IL-1RA  LLFLFHSETI  CRPSGRKSSK  IQAFRIWDVN  QKTFYLRNN.  QLVAGYLQGP
  IL-1_delta  ----------  -----MVLSG  ALCFRMKDSA  LKVLYLHNN.  QLLAGGLHAG
        CS329  ----------  ----MCSLPM  ARYYIIKYAD  QKALYTRDG.  QLLLVGDPVAD
     Tango-77  SLPTMNFVH.  .T........  ..........  ..........  ..........
       Zilla4  SLPTMNFVH.  .TSPKVKNLN  PKKFSIHDQD  HKVLVLDSG.  NLIA..VPDK
   IL-1_zeta  TKGKNSFKKR  LRGPKVKNLN  PKKFSIHDQD  HKVLVLDSG.  NLIA..VPDK
  IL-1RA_beta  ..........  .......MCK  PITGTINDLN  QQVWTLQGQ.  NLVA..VPRS
     Spoil_II  VEAPAFSAPL  CTLPFFPPVCK  PITGTINDLN  QQVWTLQGQ.  NLVA..VPRS
IL-1_epsilon  ----------  ~MEKALKIDT  PQQGSIQDIN  HRVWVLQDQ.  TLIA..VPRK
     IL-1_eta  ----------  ~-MNPQREAA  PKSYAIRDSR  QMVWVLSGN.  SLIA..APLS

             151                                                  200
  IL-1_alpha  DMEQQVVFSM  ...SFVQGEE  SNDKIPVALG  LKEKNLYLSC  VLKDDK..PT
   IL-1_beta  DMEQQVVFSM  ...SFVQGEE  SNDKIPVALG  LKEKNLYLSC  VLKDDK..PT
       IL-1RA  NVNLEEKIDV  VP.....IEP  ....HALFLG  IHGGKMCLSC  VKSGDE..TR
  IL-1_delta  KVIKGEEISV  VPNRWLDASL  ....SPVILG  VQGGSQCLSC  .GVGQE..PT
        CS329  NC.CAEKICT  LPNRGLDRTK  ....VPIFLG  IQGGSRCLAC  VETEEG..PS
     Tango-77  .....KIFFA  LASSLSSA.S  AEKGSPILLG  VSKGEFCLYC  DKDKGQSHPS
       Zilla4  NYIRPEIFFA  LASSLSSA.S  AEKGSPILLG  VSKGEFCLYC  DKDKGQSHPS
   IL-1_zeta  NYIRPEIFFA  LASSLSSA.S  AEKGSPILLG  VSKGEFCLYC  DKDKGQSHPS
  IL-1RA_beta  DSVTPVTVAV  ITCKYPEALE  QGRGDPIYLG  IQNPEMCLYC  EKVGEQ..PT
     Spoil_II  DSVTPVTVAV  ITCKYPEALE  QGRGDPIYLG  IQNPEMCLYC  EKVGEQ..PT
IL-1_epsilon  DRMSPVTIAL  ISCRHVETLE  KDRGNPIYLG  LNGLNLCLMC  AKVGDQ..PT
     IL-1_eta  RSIKPVTLHL  IACRDTEFSD  KEKGNMVYLG  IKGKDLCLFC  AEIQGK..PT
```
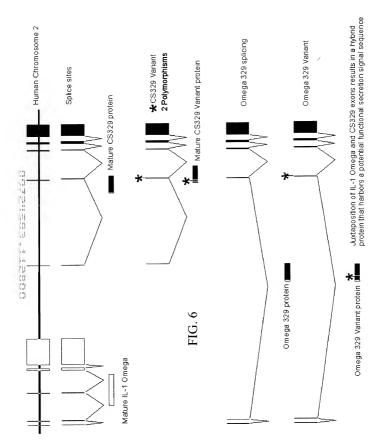
FIG. 4B

```
             201                                                    250
 IL-1_alpha  LQLESVDPKN Y..PKKKMEK RFVFNKIEIN NKLEFESAQF PNWYISTSQA
  IL-1_beta  LQLESVDPKN Y..PKKKMEK RFVFNKIEIN NKLEFESAQF PNWYISTSQA
     IL-1RA  LQLEAVNITD LSENRKQDKR .FAFIRSDSG PTTSFESAAC PGWFLCTAME
 IL-1_delta  LTLEPVNIME LYLGAKESKS .FTFYRRDMG LTSSFESAAY PGWFLCTVPE
      CS329  LQLEDVNIEE LYKGGEEATR .FTFFQSSSG SAFRLEAAAW PGWFLCGPAE
    Tango-77 LQLKKEKLMK LAAQKESARR PFIFYRAQVG SWNMLESAAH PGWFICTSCN
     Zilla4  LQLKKEKLMK LAAQKESARR PFIFYRAQVG SWNMLESAAH PGWFICTSCN
   IL-1_zeta LQLKKEKLMK LAAQKESARR PFIFYRAQVG SWNMLESAAH PGWFICTSCN
 IL-1RA_beta LQLKEQKIMD LYGQPEPV.K PFLFYRAKTG RTSTLESVAF PDWFIA.SSK
    Spoil_II LQLKEQKIMD LYGQPEPV.K PFLFYRAKTG RTSTLESVAF PDWFIA.SSK
IL-1_epsilon LQLKEKDIMD LYNQPEPV.K SFLFYHSQSG RNSTFESVAF PGWFIAVSSE
    IL-1_eta LQLKEKNIMD LYVEKKAQ.K PFLFFHNKEG STSVFQSVSY PGWFIATSTT
```

```
             251                                          290
 IL-1_alpha  ENMPVFL... .GGTKGGQDI TDFTMQFVSS ----------
  IL-1_beta  ENMPVFL... .GGTKGGQDI TDFTMQFVSS ----------
     IL-1RA  ADQPVSLTNM PDEG...VMV TKFYFQEDE- ----------
 IL-1_delta  ADQPVRLTQL PENGGWNAPI TDFYFQQCD- ----------
      CS329  PQQPVQLTKE SEPSAR.... TKFYFEQSW~ ----------
    Tango-77 CNEPVGVTDK FENRKH.... IEFSFQPVCK AEMSPSEVSD
     Zilla4  CNEPVGVTDK FENRKH.... IEFSFQPVCK AEMSPSEVSD
   IL-1_zeta CNEPVGVTDK FENRKH.... IEFSFQPVCK AEMSPSEVSD
 IL-1RA_beta RDQPIILTSE LGKSYN.... TAFELNIND- ----------
    Spoil_II RDQPIILTSE LGKSYN.... TAFELNIND- ----------
IL-1_epsilon GGCPLILTQE LGKANT.... TDFGLTMLF- ----------
    IL-1_eta SGQPIFLTKE RGITNN.... TNFYLDSVE- ----------
```

Phylogenetic Tree of the Emerging IL-1-ra Gene Family

FIG. 5

FIG. 6

FIG. 7

```
atg tgc tcc ctt ccc atg gca aga tac tac ata atc aag gat gca cat    48
Met Cys Ser Leu Pro Met Ala Arg Tyr Tyr Ile Ile Lys Asp Ala His
 1               5                   10                  15

caa aag gct ttg tac aca cgg aat ggc cag ctc ctg ctg gga gac cct    96
Gln Lys Ala Leu Tyr Thr Arg Asn Gly Gln Leu Leu Leu Gly Asp Pro
               20                  25                  30

gat tca gac aat tat agt cca gag aag gtc tgt atc ctt cct aac cga   144
Asp Ser Asp Asn Tyr Ser Pro Glu Lys Val Cys Ile Leu Pro Asn Arg
           35                  40                  45

ggc cta gac cgc tcc aag gtc ccc atc ttc ctg ggg atg cag gga gga   192
Gly Leu Asp Arg Ser Lys Val Pro Ile Phe Leu Gly Met Gln Gly Gly
     50                  55                  60

agt tgc tgc ctg gcg tgt gta aag aca aga gag gga cct ctc ctg cag   240
Ser Cys Cys Leu Ala Cys Val Lys Thr Arg Glu Gly Pro Leu Leu Gln
 65                  70                  75                  80

ctg gag gat gtg aac atc gag gac cta tac aag gga ggt gaa caa acc   288
Leu Glu Asp Val Asn Ile Glu Asp Leu Tyr Lys Gly Gly Glu Gln Thr
                85                  90                  95

acc cgt ttc acc ttt ttc cag aga agc ttg gga tct gcc ttc agg ctt   336
Thr Arg Phe Thr Phe Phe Gln Arg Ser Leu Gly Ser Ala Phe Arg Leu
               100                 105                 110

gag gct gct gcc tgc cct ggc tgg ttt ctc tgt ggc cca gct gag ccc   384
Glu Ala Ala Ala Cys Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro
           115                 120                 125

cag cag cca gtg cag ctc acc aaa gag agt gaa ccc tcc acc cat act   432
Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Thr His Thr
     130                 135                 140

gaa ttc tac ttt gag atg agt cgg taa                                459
Glu Phe Tyr Phe Glu Met Ser Arg
145                 150
```

FIG. 8

```
  1 MCSLPMARYYIIKYADQKALYTRDGQLLVGDPVADNCCAEKICTLPNRGL 50
    ||||||||||||| | |||||||·||||·||| ·|| ||:| |||||
  1 MCSLPMARYYIIKDAHQKALYTRNGQLLLGDPDSDNYSPEKVCILPNRGL 50

 51 DRTKVPIFLGIQGGSRCLACVETEEGPSLQLEDVNIEELYKGGEEATRFT 100
    ||·|||||||·|||| |||||·| ||| |||||||||:|||||: ||||
 51 DRSKVPIFLGMQGGSCCLACVKTREGPLLQLEDVNIEDLYKGGEQTTRFT 100

101 FFQSSSGSAFRLEAAAWPGWFLCGPAEPQQPVQLTKESEPSARTKFYFEQ 150
    ||| | |||||||||| |||||||||||||||||||||||| |·|||
101 FFQRSLGSAFRLEAAACPGWFLCGPAEPQQPVQLTKESEPSTHTEFYFEM 150

151 SW 152
    |
151 SR 152
```

FIG. 9A

```
actagtctcc catagacaac agctgaatgt acgaggtcag aagcaaggcc tgccccagaa  60

ccattgcaag ccaggtgctg tcttgattgt agcctcataa aaaactgatg cagaattgcc  120

ccaccaacat gctccagatt cctgctccac agaaaccctg tgaactaacc atgttgcttt  180

tagattctgc agtaagttga taatctgcag taaataacat tcgatgaaag agaaacatgt  240

gtagttactt tattatgatc aaaactttat ttctccactc tttccatttt ccttctcaga  300

attgacacca gcctttcact aacccaaata gcctatttaa atgctgatca tacttctctt  360

gttaactgtt acctgttccc aaaaggtaca attcccttc gaccatagct gcatctccca  420

cctgcacacc aggatgtttc tcatatttct acctaaaaca ttggggacta caagtgaaag  480

caaaagaggg ggtccatatc agaaccccag gtatttagct gtaaaactca cttgtcaggc  540

cagcttgaca ggtttacagt ttgtagaagg accagaaaga aggtagccaa gacagaagag  600

gcaacctctg cttgtcctag aaccttcagt ccatatacat ctaagctccc cagcaccatt  660

tctaccacag acctctcaga gttcctgagg atgcagaccc caggacactg acctcagttt  720

ccaggcaggg tttctgcaca cccccttcac actgcctgac tgggagttag tctcatggtg  780

caacactact ttgggacact gtacccatcc cctcgaccta cagaaaccat tcacttttca  840

aggtcacctc ctataggaag tatttgaaaa gatgagagtc atggtcattt gctatgataa  900

tattctgtgc ttatctccct gtaaaaagtt ggcttggggt ctctggcatg catctgacct  960

taaggttgga gctgcaccaa tatgtttta agcacccggc ataatgcttc gcaaaatttc  1020

agaacatggt ttgtacagaa tgtactttcc tccactcata caaacccttg taaaagagta  1080

gtttgaatcc caactcattc ttgaaggcca cctttgtag ggtgacagaa tttaaaaata  1140

cagaatttaa aaatactta tcccagggaa gctcacactt ctaaatccag aatgaaagaa  1200

gaaatagaaa cacacttgtg gtggcggtgg tggtggtgat ggtggtcgtg gtggtggtgg  1260

tggtggtggt ggtgatggtg gtggtggtgg tggtggtggt ggtcgtggtg gtgtaatgat  1320

cacagtaaag tgaggcatca tggcctgaga gagtcaggca tcacagctat tcaagtgaaa  1380

actacctact actgatttta gagttctata attttagtag cagccacagg cctggggcct  1440

gggcctatat tttcagagag gaaatgttca cagcaggtca actgcagaca gtgaagatca  1500

gaaatgtttc ataatcaggt catcagagaa aaggcaaagg agctgatgga ctttatcctg  1560

aaaaagcaaa atccaaccca cctcatgctt aatgcattca aaggtctgcg ggcagaagaa  1620
```

FIG. 9B

```
tacattttgc tttttattat tataaattac ctggagaata tttttgtctg aattatctcc 1680

caaatattaa ccataaaaat aaaaaattcc atgtgtgctt ctcccagggg ctataaagcc 1740

cctggtctta gagttgttgg ggcaaaacct gacctttgaa gtagttactt ttgaagatgc 1800

cataccatac atttggccac ttggagagag tctaatgtca catctaaagg gttactctga 1860

tgctctgttt tctcatatgc ccttggctta cagctaacta tggctccagc taaactataa 1920

agttccttgg caacagagat ggtacgctat gtgtctttga cacagcagaa taaatgctta 1980

gtgaacatta ctgattgcct gacaggacac ctcacacttt ggtactttca acagagggat 2040

gtaaacttat gaagaacaat gaagaatgaa tattggcaat aaaagcaaaa attggttaac 2100

ccaattctag ctctgaaatc attttttaggt agtgggaagt ctttttgttt tgtttattca 2160

ctttacatcc caattgctgt cctccctcca agttccccac caccaccaca gtcctttttc 2220

cctcccccttc tcctctgaga gaatggagaa ccctcctgga tattccccca tcatgaaaca 2280

ttaagtctct gcagggctag acacttcccc cagtgaggcc agtcagggca gcccagctag 2340

aaaaagcata tcccacagac agacaacagc ttttgggata gccccgttcc agttgtttag 2400

gatccacatg aaggctgagc tgcacatctg ctacatatga atgaggaggc ctaggtccag 2460

cctgtgtatg ttctttggtt ggtggttcag actctgagag ccccaagggt ccaggtcagt 2520

tgactctgtt ggtcttcctg tggacaccct gtccccttcc agcccacaat ccttccccta 2580

atccttctcc ttctcacttc cataagagtg tgaggagtct ttaaaaacat gaagcatttt 2640

atctccccag ggcaacacat ggaaatgaaa gattgtgaaa agtaatttaa agaaaaagaa 2700

aaaaaaattt aacaaggaat aagaatcttg tttctctgaa aatgcttaag agtgtggaaa 2760

acataaactg gattctaata gaatgcaatt ggattgtaat gaaaacctat caaagttatg 2820

aaatagcttt cactaccttg cacaaaatct cttggcatgt gtgttgttgg caaattttct 2880

tgttagttta aaaccacaac aataacaaca aaatagcaaa aattgggtct cagcctcatt 2940

catttttct catttcttgc tctgtgatcg tctgggtctt aagctgacac ctcaccaatt 3000

cctcatcaag accctttgtgg aaatttgcaa atgtcccaaa aaggagaatt acaataagtc 3060

agagaacgtt ctgtccaatt ctttatccct agtgatggat gagtaaagga tgtataagag 3120

atggataaat ggactgatgt acagataaat gaaggaatat gtacatggtt aggtggatag 3180

atgacttact caacagatga gtagaaggat gagaaataga tggacagctg gactgaggca 3240
```

FIG. 9C

```
tgcaaagtca actggagaac tgagtctctt gaccatgcac tgtccagggt ctcatattcc 3300

ctagagtcca gggcccatgg ctcctgtgcc atccccatgc aaatctaagg ttaatacgtt 3360

ctacagctga gtttccttac atatgtgtct cagtaagttt gtatcaacta attaaatctg 3420

aaaggagttc cttctgatct tcccaaacag agccacactc gtgatgaagt cagccctgct 3480

tcattgtggt tctctggatg catctggctt ccatcagcat aatctttcta ttcttgatcc 3540

ttccaacctc ttcaggtctc agacagaacc ccatggagca tcaaagaggt ttgaccccag 3600

cattgtttat gtagctgcaa aaccactaat aacacagtca atgacagtag ctacagagac 3660

agcaggtcag tgtctggcct ctgtcaaggc tttatgagtg actctctccc cttcccgcaa 3720

atactcatta atctccccac ctccttatta tttggactgt gttgaagata ttatgaaatc 3780

tctgggctct tcttcccgga tctagagcca attacagatt ctgtaggttt gacccaccct 3840

gaccagacat tataaacaca gtgctggtgc cctgaagaaa acagttggag actccaggca 3900

ttagaatcca ggcaccagga actacaggtc agtggtgaca gtcggtctct ctgtgtatct 3960

cttacacaca cacacataca cacacacaac acaacataca cacacataca acacacaaca 4020

catacacata caacacatac acacacacaa cacttttctg taatgtctcc aaaattctca 4080

ggctctaggg aagaagaaat gtctttagga gaatgcggtg tgatgttcta taagtctagg 4140

aatacttgat agaatttaat gagaagtata gattaggtca aagcaagggt actacatatt 4200

tggaaccaca gagtttgaa agtcatctca aaagaaatta tttaggccag agatgttcaa 4260

aaaatgtttt gtttgtgaca tatggaagct cccatggaga cattctgtga ttctcatcaa 4320

tagacagtag ggatgccacc aaggtgctaa cgtcttcatc accccatcat ctatcataca 4380

tccaaatggt ttctttgaaa acaatctcct tgtgaaactt aaagtagcct tgaaaatata 4440

ataatcttgt ccagcctctc atttcaatgg gaatagattg aaggcctaag gaccaaaaca 4500

aaaaacaaaa caaacaaaat aaaaacacca aaaaaaaaac ccataaaatg aatgagtagc 4560

taagttattt ttagaatcca gcctttcagt caaagcttga ttcatgcata tctgtgttct 4620

gatcttaagg tgctgtgtct gtcagttgta tagttggata gaggtacaga tgagctatat 4680

acatcatgct tcaagatttc aggatcttat aactttttata aagcaaataa tttgtcttaa 4740

tgcacactaa taaacaatat agcaaagttt gacaggagtt cagagtactg ttagagaagt 4800

gaagggaaga attttgttat gatagtaaag gggaaaatca aattttgagt catggaatca 4860
```

```
tacatagttt gacatagaaa gaaccttggc aaccacataa tctaatgcat gagcccaaga 4920

actggcctgt gtttttaaga tctcattctc agctgttatg taactgaaca gacaagatac 4980

taagcccaag tatagtgaag ccatgtccag tgatcttaat aggagtgaca ggaatggttg 5040

gtgatgaaga ggggtggatt ttgagcagga ataccaaaag caatgctgac tgtgcccttg 5100

gagagaatta gcatgagtcc ttgagagaaa aatgagatgc tattgcacaa gcaacctagg 5160

gccagatggt gtcaagatag gtggccatcg tggactttag aaccaggcag gaatgtgatc 5220

agagatgtac tttatgtagg ttaggtttga ttcagaaacc aggagggtta gcatgtttac 5280

aatggtgact aaaaacaagc acaaggttat actttaaaga aataatctct gaaaagaagg 5340

gaggtatatt ttcagtgccg gaaagaggaa tattacaaaa gtgagaggag tagatttgag 5400

aaagagaagt ggattgtgga ggagcagatg ctcaccacgc ccttacactc acttgaactg 5460

acacccaaag atgaaggtgt gctgtggact gctgaagctc agcctgtggc tgggaagcag 5520

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cttaggctat tctcttacaa ctctcagcct tatgaatgac ccggaaggaa aagaactcta 5640

caatgtgcct gtgtctgttc ttacttcctc tgccacaagc aaaagagcct tgggaattgg 5700

ctcagaggga acgtcatcaa acaggctggc cttgaggctg ggctgttatt cgtctacctg 5760

ggatagagga attcgctatt cttttataat ccaagtgtgg cctggggacc agcagcatta 5820

ttaagacctg gttgcatgtt tgaaatgcag tctcagattt catcccagac ctaaagagta 5880

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gggtaaatgt catgcaagca ggaggatctg attgactccc caggacccac acagttccca 6000

tgccgtagag cacatctgta atcacagtag gcgtatgatg aaatgggagg tgaatcaaga 6060

gaatctctag cagctacggg ctggccagcc tcccatgcac agcactaaat aaggcaagga 6120

ccaatacctg aagttgtccc attaccttca catatacacc acggcatgtg tgtacttgta 6180

ctcacacata caaacaaata cacacgtgca cacatacaaa actcagagat taaggacaat 6240

tggcctgaca tatcagttcc taagcctggc tcattgcttg taacactaca agcagtatta 6300

aataaggata ggcgagagaa cagttaccga atggttcaga agtggggcca tgcctgtgac 6360

tttaaacaaa tgtttcatat ttttaaataa taacacttag attacaaaat aaatttacta 6420

caggaaaatg ttaagaacta tcaacaacca ttgactatcc tgtcggccac aaatgagtgt 6480
```

```
tataacaagc accagccgtc cttgtccaca tgtgtgtgtg tctacacagc tatgaattta 6540

attgggataa taatgtgcac attctttacg gcctgcagtt tttacttcat gtatttgaaa 6600

tgtttgtgcc acaaatgtca tctttaagga gcatatcctt atttcctgga tttatcattc 6660

cctttcagcc gactggdact tgacagcatt tccaactttt caaccttgta aaaataacta 6720

attgaactat tttataacta agcatttggg caatcaatta cctctgcctg gaatgggggc 6780

aacaacacat gcaatcatgg gaaagccagg atgctgctgt ctgatcccta gccctggcat 6840

tcgtgcagaa cctcactctc atctgtgccc tgatatcctt cactctcaag tcttttccca 6900

gtgacttta aaggcaacag aatcatatag ccaataatga aagctacttg gtctacagtt 6960

gtgtggcgtt ttttatagat attttcttca tttacatttc aaatgctatc ccaaaagtcc 7020

cctatacct ccccacct gctcccctac ccactcactc ccacttcttg gccctggctt 7080

tccccttac tggggcatat aaagtttgct agaccaaggg gcctctcttc ccaatgatgg 7140

ccaactaggc cattttctgc tacatatgca gctagagaca ccagttctgg ggttactggt 7200

tagttcatat tgttgttcta cctatgggt tgcagaccc ttcagctctt gagtactttc 7260

tctagctcct ccattgggag ccctgtgttc catcctatag atgactgtga gcatccactt 7320

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tggaccccg ggtggggcag tctctggatg gtccatcctt tcatcttagc tccaaacttt 7440

gtctctgcaa cttcttccat ggatatttta gtccctaatc tagggagaaa tgaagtatcc 7500

acaagttgat cttccttctt gattttctta tgttttagaa gttgtatctt ggatattcta 7560

ggtttctggg ctaatatcca cttatcagtg agtacatatc aagtgaattc ttttgtgatt 7620

aggttacctc actcaagatg atattctcca ctatgttcat agcagcccta tttatagtag 7680

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aaaccctatc taaagaccag gaataaggaa aagatggact gcctgcctgc agctgggaga 7860

gctggggaga cctttgtgga ttctgtaata cttaggggta cggaacagct tgtggctgga 7920

taattctgag ctccagcatg tctgcccccc aaaaaacatt ctgtttttct gaaagccttt 7980

ttcttctttg cctcagtgaa gaccagacac tcccaactgc agga atg tgc tcc ctt   8036

ccc atg gca aga tac tac at gtaagtaa tcttaacgat cgctcaatca           8084
```

FIG. 9F

```
aggggcctgg agatcacatg agaagggaaa aggctgagtc aaagggacaa agctccctct 8144

agccacagaa atctcaaaca ctgaataatt gatcttcatc tttgtcaatc acaacagccc 8204

tctttcctgg tgacagaatg gaacaactgt aagagtggta ttgcttagtc cattttacag 8264

acccggaaac tcaacctcca cgaggttata caatttcct catgtcatgc aattacccaa 8324

aagcagagag tgggatcgga ctctctgttc tctaaactga tgtagctagt cttagaaag 8384

ctcaaacaat cttgagtccc aaggacagca cctttatggt cacctggatt gatacctata 8444

tcaaaaaaa aaaaaggtct cactagatag ccctggctac cctgaaactc tcactgtgta 8504

catttaggtg accacgaact cacagagatc tgccttccaa gtgctgggat taaagtatgt 8564

accaccacac ctgcatcttt gacaataact gagtggtatc taaattcttc cagtggctaa 8624

acagttaagt cccagttccc aaagtctgag aaaaatgcca ggtggtgaaa tctgtacaga 8684

cctttgttct taatgtacaa gtgagcctgc tttaaaaaca atacgcaagc tgttttgct 8744

attgctaagt gttgcagaga cagaaaaggc tcccagaagt ggtaactttg gtccagaggt 8804

tctgttctca aactcattgt gagctctgaa agcaactgat gggcagctct gaaatcagct 8864

gggcaattag gctaataaca ggcataattt taatgtttca cacgcatgac agttcctccc 8924

cagctgccct agtacatact taccctccta ggcacgtcat tagacccata ggtataacca 8984

gtgactaatc aggccctggt ctaattctaa gttggcctcc tatataagtg ccactcagag 9044

tgtacctcat catggctgta gtgggcccag agtctaggga catagacttt tctattgtcc 9104

aatttctgat ttgtgaattt tctacaaaaa gaattttttt taattttaca aatcaaatca 9164

cagttactac atcttcagtt ccttcattaa ttagtgttac tatttaaaaa aataaaataa 9224

atcaagctca gaaacatcat ggatagggtt cattgtatct ccagggtacc tgagcttcaa 9284

agcaactcct cagacagcca tgaaaacatc ctcaattacc tcatgagaag acactattgt 9344

catttctgga gcctctgata atcctgagcc taggcagctt tgggatgaaa caatttctac 9404

ccttattgga acagtgtccc tctcctgtct ggaaacaatt caccaaaggc tccatgtggt 9464

tgtccagtaa ggtggtatgg ggacagaaat ggacaatgat ccctgagggc agtgatccat 9524

taaccttgcc ctcctatttc ag a atc aag gat gca cat caa aag gct ttg tac 9577

aca cgg aat ggc cag ctc ctg ctg gga gac cct gat tca gac aat tat    9625

agt cca g gtgatcttc cggtggtggg ggtgggggag tggaggggag ggtgtggggg    9681
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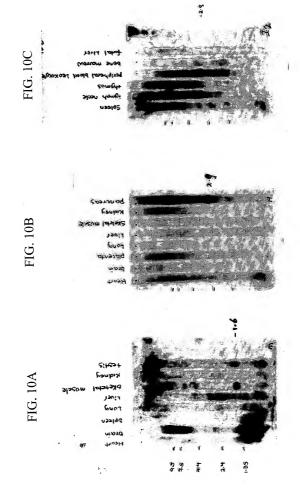
FIG. 9G

```
gggctctctt ccagaagttg cttagtgtcc atctgccaca aggccttgat tctttccttc 9741

aattgtgtct ctagagacat gagaatattg tcacagtgat aaggagaaga ggtaggggca 9801

gtttcttcct gtaaaaaatg aattccattt accctgcagt ctccatacag aaacaggcca 9861

gaggggggca gacccagtaa cttctagctg agccctacct tgcttaaaac ctgccatctg 9921

tggtcccctc actgtctgaa ttgcattctg tcttacctcc cag ag aag gtc tgt atc 9978

ctt cct aac cga ggc cta gac cgc tcc aag gtc ccc atc ttc ctg ggg     10026

atg cag gga gga agt tgc tgc ctg gcg tgt gta aag aca aga gag gga     10074

cct ctc ctg cag ctg gag gtgagacacc cctcctcatt gcagtcagta           10122

ctgccactgg aacatagtga catctttgaa cccacatgtc ccctctcttg tttcccatct 10182

atctctcttt gcctccagct gagggactct agcctttggg gatgtacaga aagaacatgg 10242

cttcggaaaa ctcttcccta ttgagtcctt ctttggccaa gcctctgagg cactaagggc 10302

tgacgtccca accaaacact catttcatct cacagctgtc tccctttccc cacag gat  10360

gtg aac atc gag gac cta tac aag gga ggt gaa caa acc acc cgt ttc     10408

acc ttt ttc cag aga agc ttg gga tct gcc ttc agg ctt gag gct gct     10456

gcc tgc cct ggc tgg ttt ctc tgt ggc cca gct gag ccc cag cag cca     10504

gtg cag ctc acc aaa gag agt gaa ccc tcc acc cat act gaa ttc tac     10552

ttt gag atg agt cgg taa agagacataa ggctggggcc tcgtctagtg           10600

ccccagtct gagatcttct tgctcagcat ctctggaaag cagaataagg aagataccaa 10660

agatgtttgg gtcttaatcc ccagaatctg tgaccgtgtt acattaaatg gcaaagggat 10720

ttttttttc cttcatggtc catttgggcc cattggaatc atctgaggcc tcatgaggag 10780

aaggaagagg tcagagggag actggggcaa actttggtac taaaagtaac aatggagaca 10840

gggaccataa gctgatgggt aacagtggtt tctagaaacc ggaaatgatg agagctctcc 10900

tgacacaggt tctggatttt tctggactga agaatggtga aataatacag ctccattatt 10960

ttaagccact gagtttgaga tcattcaatg aagctgtcat aataaaacct gtgcttcaca 11020

tacaattcaa tattggtagg caccccggtg atttcttgga aagacatcta gggattctcc 11080

tggatgctga ttccagggtc cagtggagtc cctgggttga agagatttca caacccagaa 11140

catcaggctc gactcttcta aaagtccgtc gttgcacccc ttgcctgaga gcattagcaa 11200
```

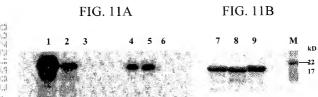## FIG. 9H

```
tttctatttc ataggaaatc tgtgtccctg cccctgctaa agcagggagc ctggaccgtc 11260

ctgatttagt gaggggtgag ctgctggcac ttttttgtgt caccagtgtc ttaagcagtg 11320

atggagcaca aaagatcttt actgagaaga tggccatgaa gctctggcta gacaccaaga 11380

atatgatata agcagagcta cagcacaaga tgagccaatg aggaaagcca ttcagggagg 11440

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ggcagagaac ataggtcaag cattctaggt agaatcagca attcagaaag gtgtgagaga 11560

ggcatggaga gctccaggca tgtctgggct atggtgtgtc attcttgtgg caagaatcca 11620

acgtctgtgg ttaaggagtt gctgaaaatt aaaataggaa aatgggtaga gtctaattgt 11680

gaatgacttg caaaggagtt tagcccataa gtgggggagct cagaggagtc atctaaggat 11740

tgcaagcagg ggccctgtga tcattgctgg accagcctag gtgctacaga gcctaccttc 11800

agctctgcat cctcactcac atccaggtac cttcagaggt caatttctgt gctctggttc 11860

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gctttaccaa gggggcactg attggagaat tggaatgagg gtggttagaa tgcattcaga 12040

aaacaagggg aagaaaaatt tgattgctta aagtggaaag tcccaactta aatgttagtc 12100

agtagtttct aattacttga gtctctaatt agaggttagt tggcagtttc tggttagtta 12160

atctaagttt cattttctta ggctatgacc attctctgag tcgcatgtta gcaatgcagt 12220

aagaactcaa gacccagaat agcctctgtt aattatttta gcaatgatca ctcatttctg 12280

ttgcctccta ttgagatctg ttcccatgga ccacccaggc acatcaggcc tcctagtacc 12340

aacataataa tgattgctgc acagacaaaa tattttttt cagtatctgg tatttgctac 12400

atttccatta gtgctggagg gaaggctaca acgaccatga aggcatggcc cctgccttct 12460

aaggacttac aatgtaatag gagccctgac attataaagt gggtcacctt gtttcaaact 12520

gagccaaact gaggctgagg gcttagatta gtggtaggtc actttccaga catgttcagt 12580

gctaagaaaa acacattctg gggttagtta gatgtttttag ttcatttgat aagaagccca 12640

atgattggac tttcaacttc tggaacccat gtggtggaag agagaaccaa cttctgacca 12700

tttgggtcat ggcacatccc ctaccatcac aagaactcac caaaataaat tagaaaaatc 12760

aagaaaaact catatcctat agacctctgg tagaattagc agaacgctgc tgtggcactt 12820
```

FIG. 9I

```
gggatttgaa actcaaaaat ggaagaagct acttgtgacc gttcaagact ccagggaggc 12880

tcctctgaca catcccacga ctcaggctta aattccttct tctccctaga aggccacgcc 12940

atcttctcaa ccaggccaca gatgctataa ttatgtaaat gtgtgggaga ggcacacttt 13000

agatcttatc cactagt                                                 13017
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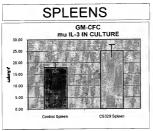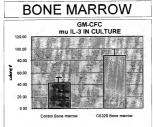
FIG. 10A

FIG. 10B

FIG. 10C

FIG. 11A   FIG. 11B

FIG. 12

Spleen

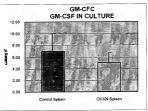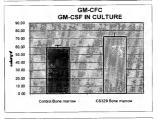|	CD4+	CD8+	CD4+ CD8+	CD3+	NK1.1+	CD3+ NK1.1+
control mice	20.18	3.72	1.67	24.07	3.06	1.4
CS329 mice	15.89	3.99	0.37	22.9	2.08	1.1
Difference:	-4.29	0.27	-1.3	-1.17	-0.98	-0.3

Bone Marrow

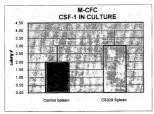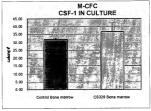|	CD4+	CD8+	CD4+ CD8+	CD3+	NK1.1+	CD3+ / NK1.1+
control mice	2.62	2.54	0.49	3.88	1.26	0.49
CS329 mice	2.46	2.35	0.41	4.42	1.53	0.57
Difference:	0.16	0.19	0.08	0.54	0.27	0.08

FIG. 13A

SPLEENS

GM-CFC
mu IL-3 IN CULTURE
Control Spleen / CS329 Spleen

GM-CFC
GM-CSF IN CULTURE
Control Spleen / CS329 Spleen

M-CFC
CSF-1 IN CULTURE
Control Spleen / CS329 Spleen

BONE MARROW

GM-CFC
mu IL-3 IN CULTURE
Control Bone marrow / CS329 Bone marrow

GM-CFC
GM-CSF IN CULTURE
Control Bone marrow / CS329 Bone marrow

M-CFC
CSF-1 IN CULTURE
Control Bone marrow / CS329 Bone marrow

FIG. 13B

SPLEENS	BONE MARROW
GM-CFC G-CSF IN CULTURE	**GM-CFC G-CSF IN CULTURE**
BFU-E/CFU-MIX rSCF + Epo in culture	**BFU-E/CFU-MIX rSCF + Epo in culture**
GM-CFC/CFU-MIX Il-3 + Epo in culture	**GM-CFC/CFU-MIX Il-3 + Epo in culture**

FIG. 14

FIG. 15